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Der Präsident des Europäischen Patentamts;
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Plants having modified growth characteristics and method for making the same

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Plants having modified growth characteristics and method for making the same

The present invention relates generally to the field of molecular biology and concerns a method for modifying plant growth characteristics. More specifically, the present invention concerns a method for modifying plant growth characteristics, particularly yield, by introducing into a plant a nucleic acid encoding a CAK. The present invention also concerns plants produced by the methods according to the invention, which plants have modified growth characteristics relative to corresponding wild type plants. The invention also concerns constructs useful in the methods of the invention.

The ever-increasing world population and the dwindling supply of arable land available for agriculture fuel agricultural research towards improving the efficiency of agriculture. Conventional means for crop and horticultural improvements utilise selective breeding techniques to identify plants having desirable characteristics. However, such selective breeding techniques have several drawbacks, namely that these techniques are typically labour intensive and result in plants that often contain heterogeneous genetic components that may not always result in the desirable trait being passed on from parent plants. Advances in molecular biology have allowed mankind to modify the germplasm of animals and plants. Genetic engineering of plants entails the isolation and manipulation of genetic material (typically in the form of DNA or RNA) and the subsequent introduction of that genetic material into a plant. Such technology has the capacity to deliver crops or plants having various improved economic, agronomic or horticultural traits. A trait of particular economic interest is yield. Yield is normally defined as the measurable produce of economic value from a crop. This may be defined in terms of quantity and/or quality. Yield is directly dependent on several factors, for example, the number and size of the organs, plant architecture (for example, the number of branches), seed production and more. Root development, nutrient uptake and stress tolerance are also important factors in determining yield. Crop yield may be increased by optimizing one of the abovementioned factors, which in some cases may be done by modifying the inherent growth mechanisms of a plant.

The inherent growth mechanisms of a plant reside in a highly ordered sequence of events collectively known as the 'cell cycle'. Progression through the cell cycle is fundamental to the growth and development of all multicellular organisms and is crucial to cell proliferation. The major components of the cell cycle are highly conserved in yeast, mammals, and plants. The cell cycle is typically divided into the following sequential phases: G0 – G1 – S – G2 – M. DNA replication or synthesis generally takes place during the S phase ("S" is for DNA synthesis)

and mitotic segregation of the chromosomes occurs during the M phase (the "M" is for mitosis), with intervening gap phases, G1 (during which cells grow before DNA replication) and G2 (a period after DNA replication during which the cell prepares for division). Cell division is completed after cytokinesis, the last step of the M phase. Cells that have exited the cell cycle and that have become quiescent are said to be in the G0 phase. Cells in this phase can be stimulated to renter the cell cycle at the G1 phase. The "G" in G1, G2 and G0 stands for "gap". Completion of the cell cycle process allows each daughter cell during cell division to receive a full copy of the parental genome.

Cell division is controlled by two principal cell cycle events, namely initiation of DNA synthesis and initiation of mitosis. Each transition to each of these key events is controlled by a checkpoint represented by specific protein complexes (involved in DNA replication and division). The expression of genes necessary for DNA synthesis at the G1/S boundary is regulated by the E2F family of transcription factors in mammals and plant cells (La Thangue, 1994; Muller *et al.*, 2001; De Veylder *et al.*, 2002). Entry into the cell cycle is regulated/triggered by an E2F/Rb complex that integrates signals and allows activation of transcription of cell cycle genes. The transition between the different phases of the cell cycle, and therefore progression through the cell cycle, is driven by the formation and activation of different heterodimeric serine/threonine protein kinases, generally referred to as cyclin-dependent kinases (CDK). A prerequisite for activity of these kinases is the physical association with a specific cyclin, the timing of activation being largely dependent upon cyclin expression. Cyclin binding induces conformational changes in the N-terminal lobe of the associating CDK and contributes to the localisation and substrate specificity of the complex. Monomeric CDKs are activated when they are associated with cyclins and thus have a kinase activity. Cyclin protein levels fluctuate in the cell cycle and therefore represent a major factor in determining timing of CDK activation. The periodic activation of these complexes containing cyclins and CDK during cell cycle mediates the temporal regulation of cell-cycle transitions (checkpoints). Other factors regulating CDK activity include CDK inhibitors (CKIs or ICKs, KIPs, CIPs, INKs), CDK activating kinase (CAK), CDK phosphatase (Cdc25) and CDK subunit (CKS) (Mironov *et al.* 1999; Reed 1996).

In plants, two major classes of CDKs, known as A-type and B-type CDKs, have been studied to date. The A-type CDKs regulate both the G1-to-S and G2-to-M transitions, whereas the B-type CDKs seem only to control the G2-to-M checkpoint (Hemerly *et al.*, 1995; Magyar *et al.*, 1997; Porceddu *et al.*, 2001). In addition, the presence of C-type CDKs and CDK-activating kinases (CAKs) has been reported (Magyar *et al.*, 1997; Umeda *et al.*, 1998; Joubès *et al.*, 2001). Vandepoele *et al.*, 2002, identified four CAKs by a homology-based annotation

method. These CAKs were three D type CAKs (Arath;*CDKD;1*, Arath;*CDKD;2* and Arath;*CDKD;3*); and one F-type CAK (Arath;*CDKF;1*).

The ability to influence the cell cycle of a plant, and to thereby modify various growth characteristics of a plant, would have many applications in areas such as crop enhancement, plant breeding, in the production of ornamental plants, aboriculture, horticulture, forestry, the production of algae for use in bioreactors (for the biotechnological production of substances such as pharmaceuticals, antibodies, or vaccines, or for the bioconversion of organic waste) and other such areas.

It has now been found that introduction into a plant of a CAK-encoding nucleic acid gives plants having modified growth characteristics. Therefore according to one embodiment of the present invention there is provided a method for modifying the growth characteristics of a plant, comprising introducing into a plant a nucleic acid encoding a CAK.

Advantageously, performance of the methods according to the present invention result in plants having a variety of modified growth characteristics, especially increased yield, particularly seed yield. More specifically, such modified growth characteristics include increased aboveground area, increased number of filled seeds, increased seed weight, increased harvest index and increased thousand kernel weight (TKW).

The term "increased yield" as defined herein is taken to mean an increase in any one or more of the following, each relative to corresponding wild type plants: (i) increased biomass (weight) of one or more parts of a plant, particularly aboveground (harvestable) parts, increased root biomass or increased biomass of any other harvestable part; (ii) increased seed yield, which includes an increase in the biomass of the seed (seed weight); (iii) increased number of (filled) seeds; (iv) increased seed size, which may also influence the composition of seeds; (v) increased seed volume, which may also influence the composition of seeds; (vi) increased harvest index, which is expressed as a ratio of the yield of harvestable parts, such as seeds, over the total biomass; and (vii) increased thousand kernel weight (TKW), which is extrapolated from the number of filled seeds counted and their total weight. An increased TKW may result from an increased seed size and/or seed density.

According to a preferred embodiment of the invention, the increase in yield encompasses an increase in yield on a seed level as defined in any one or more of (ii) to (vii) above.

Taking corn as an example, a yield increase may be manifested as one or more of the following: increase in the number of plants per hectare or acre, an increase in the number of ears per plant, an increase in the number of rows, number of kernels per row, kernel weight, thousand kernel weight, ear length/diameter, among others. Taking rice as an example, a yield increase may be manifested by an increase in one or more of the following: number of plants per hectare or acre, number of panicles per plant, number of spikelets per panicle, number of flowers per panicle, increase in the seed filling rate, increase in thousand kernel weight, among others. An increase in yield may also result in modified architecture, or may occur as a result of modified architecture.

According to a preferred feature of the present invention, performance of the methods of the invention result in plants having modified yield which is manifested by at least one of: increased aboveground area, increased TKW, increased number of filled seeds, increased seed weight and increased harvest index, each relative to control plants. Therefore, according to the present invention, there is provided a method for increasing plant yield, which method comprises modulating expression in a plant of a nucleic acid encoding a CAK and/or modulating activity and/or levels in a plant of a CAK polypeptide.

Since the transgenic plants according to the present invention have increased yield, it is likely that these plants exhibit an increased growth rate (during at least part of their life cycle), relative to the growth rate of corresponding wild type plants at a corresponding stage in their life cycle. The increased growth rate may be specific to one or more parts of a plant (including seeds), or may be throughout substantially the whole plant. A plant having an increased growth rate may even exhibit early flowering. The increase in growth rate may take place at one or more stages in the life cycle of a plant or during substantially the whole plant life cycle. Increased growth rate during the early stages in the life cycle of a plant may reflect enhanced vigour. The increase in growth rate may alter the harvest cycle of a plant allowing plants to be sown later and/or harvested sooner than would otherwise be possible. If the growth rate is sufficiently increased, it may allow for the sowing of further seeds of the same plant species (for example sowing and harvesting of rice plants followed by sowing and harvesting of further rice plants all within one conventional growing period). Similarly, if the growth rate is sufficiently increased, it may allow for the sowing of further seeds of different plants species (for example the sowing and harvesting of rice plants followed by, for example, the sowing and optional harvesting of soy bean, potatoes or any other suitable plant). Harvesting additional times from the same rootstock in the case of some plants may also be possible. Altering the harvest cycle of a plant may lead to an increase in annual biomass production per acre (due to an increase in the number of times (say in a year) that any particular plant may be grown and

harvested). An increase in growth rate may also allow for the cultivation of transgenic plants in a wider geographical area than their wild-type counterparts, since the territorial limitations for growing a crop are often determined by adverse environmental conditions either at the time of planting (early season) or at the time of harvesting (late season). Such adverse conditions may be avoided if the harvest cycle is shortened. The growth rate may be determined by deriving various parameters from growth curves plotting growth experiments, such parameters may be: T-Mid (the time taken for plants to reach 50% of their maximal size) and T-90 (time taken for plants to reach 90% of their maximal size), amongst others.

Performance of the methods of the invention gives plants having a modified growth rate. Therefore, according to the present invention, there is provided a method for modifying the growth rate of plants, which method comprises modulating expression in a plant of a nucleic acid encoding a CAK and/or modulating activity and/or levels in a plant of a CAK polypeptide. An increase in growth rate is exemplified herein by an increase in aboveground area, and an increase in TKW, increased number of filled seeds, increased seed weight and increased harvest index, each relative to control plants/corresponding wild-type plants.

An increase in yield and/or growth rate occurs whether the plant is under non-stress conditions or whether the plant is exposed to various stresses compared to control plants. Plants typically respond to exposure to stress by growing more slowly. In conditions of severe stress, the plant may even stop growing altogether. Mild stress on the other hand is defined herein as being any stress to which a plant is exposed which does not result in the plant ceasing to grow altogether. Due to advances in agricultural practices (irrigation, fertilization, pesticide treatments) severe stresses are not often encountered in cultivated crop plants. As a consequence, the compromised growth induced by mild stress is often an undesirable feature for agriculture. Mild stresses are the typical stresses to which a plant may be exposed. These stresses may be the everyday biotic and/or abiotic (environmental) stresses to which a plant is exposed. Typical abiotic or environmental stresses include temperature stresses caused by atypical hot or cold/freezing temperatures; salt stress; water stress (drought or excess water). Abiotic stresses may also be caused by chemicals. Biotic stresses are typically those stresses caused by pathogens, such as bacteria, viruses, fungi and insects.

The abovementioned growth characteristics may advantageously be modified in any plant.

The term "plant" as used herein encompasses whole plants, ancestors and progeny of the plants and plant parts, including seeds, shoots, stems, leaves, roots (including tubers), and plant cells, tissues and organs, wherein each of the aforementioned preferably comprise the gene of interest. The term "plant" also encompasses embryos, meristematic regions,

gametophytes, sporophytes, pollen, and microspores, again wherein each of the aforementioned preferably comprise the gene of interest. The term plant, as defined herein, does not include suspension cultures and callus tissue.

Plants that are particularly useful in the methods of the invention include all plants which belong to the superfamily Viridiplantae, in particular monocotyledonous and dicotyledonous plants including fodder or forage legumes, ornamental plants, food crops, trees or shrubs selected from the list comprising *Acacia* spp.,*Acer* spp., *Actinidia* spp., *Aesculus* spp., *Agathis australis, Albizia amara, Alsophila tricolor, Andropogon* spp., *Arachis* spp, *Areca catechu, Astelia fragrans, Astragalus cicer, Baikiaea plurijuga, Betula* spp., *Brassica* spp., *Bruguiera gymnorrhiza, Burkea africana, Butea frondosa, Cadaba farinosa, Calliandra* spp, *Camellia sinensis, Canna indica, Capsicum* spp., *Cassia* spp., *Centroema pubescens, Chaenomeles* spp., *Cinnamomum cassia, Coffea arabica, Colophospermum mopane, Coronillia varia, Cotoneaster serotina, Crataegus* spp., *Cucumis* spp., *Cupressus* spp., *Cyathea dealbata, Cydonia oblonga, Cryptomeria japonica, Cymbopogon* spp., *Cynthea dealbata, Cydonia oblonga, Dalbergia monetaria, Davallia divaricata, Desmodium* spp., *Dicksonia squarosa, Diheteropogon amplectens, Dioclea* spp, *Dolichos* spp., *Dorycnium rectum, Echinochloa pyramidalis, Ehrartia* spp., *Eleusine coracana, Eragrestis* spp., *Erythrina* spp., *Eucalyptus* spp., *Euclea schimperi, Eulalia villosa, Fagopyrum* spp., *Feijoa sellowiana, Fragaria* spp., *Flemingia* spp, *Freycinetia banksii, Geranium thunbergii, Ginkgo biloba, Glycine javanica, Gliricidia* spp, *Gossypium hirsutum, Grevillea* spp., *Guibourtia coleosperma, Hedysarum* spp., *Hemarthia altissima, Heteropogon contortus, Hordeum vulgare, Hyparrhenia rufa, Hypericum erectum, Hyperthelia dissoluta, Indigo incarnata, Iris* spp., *Leptarrhena pyrolifolia, Lespediza* spp., *Lettuca* spp., *Leucaena leucocephala, Loudetia simplex, Lotonus bainesii, Lotus* spp., *Macrotyloma axillare, Malus* spp., *Manihot esculenta, Medicago sativa, Metasequoia glyptostroboides, Musa sapientum, Nicotianum* spp., *Onobrychis* spp., *Ornithopus* spp., *Oryza* spp., *Peltophorum africanum, Pennisetum* spp., *Persea gratissima, Petunia* spp., *Phaseolus* spp., *Phoenix canariensis, Phormium cookianum, Photinia* spp., *Picea glauca, Pinus* spp., *Pisum sativum, Podocarpus totara, Pogonarthria fleckii, Pogonarthria squarrosa, Populus* spp., *Prosopis cineraria, Pseudotsuga menziesii, Pterolobium stellatum, Pyrus communis, Quercus* spp., *Rhaphiolepsis umbellata, Rhopalostylis sapida, Rhus natalensis, Ribes grossularia, Ribes* spp., *Robinia pseudoacacia, Rosa* spp., *Rubus* spp., *Salix* spp., *Schyzachyrium sanguineum, Sciadopitys verticillata, Sequoia sempervirens, Sequoiadendron giganteum, Sorghum bicolor, Spinacia* spp., *Sporobolus fimbriatus, Stiburus alopecuroides, Stylosanthos humilis, Tadehagi* spp, *Taxodium distichum, Themeda triandra, Trifolium* spp., *Triticum* spp., *Tsuga heterophylla, Vaccinium* spp., *Vicia* spp., *Vitis vinifera, Watsonia pyramidata, Zantedeschia aethiopica, Zea mays*, amaranth, artichoke, asparagus, broccoli, Brussels

sprouts, cabbage, canola, carrot, cauliflower, celery, collard greens, flax, kale, lentil, oilseed rape, okra, onion, potato, rice, soybean, straw, sugar beet, sugar cane, sunflower, tomato, squash, tea and algae, amongst others. According to a preferred embodiment of the present invention, the plant is a crop plant such as soybean, sunflower, canola, alfalfa, rapeseed, cotton, tomato, potato or tobacco. Further preferably, the plant is a monocotyledonous plant, such as sugar cane. More preferably the plant is a cereal, such as rice, maize, wheat, barley, millet, rye or oats.

A CAK is a CDK that phosphorylates and activates CDKs. A CAK has also been shown to phosphorylate and activate RNA polymerase II. The term "CAK" as defined herein is taken to mean a nucleic sequence as represented by SEQ ID NO: 1 or SEQ ID NO: 3 and to functional variants of either as described hereinafter, or to an amino acid sequence as represented by SEQ ID NO: 2 or SEQ ID NO: 4 and to functional variants of either, as described hereinafter. The term "functional variant" is one which, in the case of a protein, retains CAK activity, i.e. the ability to phosphorylate and activate CDKs, and which, in the case of a gene, encodes a protein which retains CAK activity.

There are two known CAKs in *Arabidopsis thaliana*:

(i) CDKD which is defined herein as a CDK which binds to cyclin H and which comprises the motif NXTALRE, wherein X is any amino acid; and

(ii) CDKF which CDK does not belong to the CDKA, B, C or D family.

A CDKD may easily be distinguished from any other CDK since the motif NXTALRE is particular to this type of CDK (according to current knowledge). In contrast, according to current knowledge, an A-type CDK will have a PSTAIRE motif; a B-type CDK a P(P/S)T(A/T)(L/M)RE motif; a C-type CDK a PITAIRE motif; an E-type CDK will have an SPTARE motif; and an F-type CDK will have a XSAXRE motif.

In *Arabidopsis thaliana*, CDKDs are encoded by 3 different genes, CDKD;1, CDKD;2 and CDKD;3, each gene encoding a protein which comprises the motif NXTALRE, wherein X is any amino acid.

The nucleic acid encoding a CAK is preferably the nucleic acid represented by SEQ ID NO: 1 or SEQ ID NO: 3 or is a functional variant of either SEQ ID NO: 1 or SEQ ID NO: 3, as described hereinafter. As previously mentioned, all such functional variants of a CAK retain the ability to phosphorylate and activate CDKs.

The nucleic acid encoding a CAK is preferably operably linked to a constitutive promoter for overexpression in a plant. The constitutive promoter is preferably a GOS2 promoter, further preferably a GOS2 promoter from rice. It should be clear that the applicability of the present invention is not restricted to use of a CAK represented by SEQ ID NO: 1 or SEQ ID NO: 3, nor is the applicability of the invention restricted to expression of a CAK when driven by a GOS2 promoter.

According to a preferred aspect of the present invention, enhanced or increased expression of the CAK nucleic acid is envisaged. Methods for obtaining enhanced or increased expression of genes or gene products are well documented in the art and include, for example, overexpression driven by a strong promoter, the use of transcription enhancers or translation enhancers.

The nucleic acid encoding a CAK may be derived from any. The nucleic acid/gene encoding a CAK may be isolated from a microbial source, such as bacteria, yeast or fungi, or from a plant, algae or animal (including human) source. This nucleic acid may be modified from its native form in composition and/or genomic environment through deliberate human manipulation. The nucleic acid is preferably a homologous nucleic acid, i.e. a nucleic acid obtained from a plant, whether from the same plant species in which it is to be introduced or whether from a different plant species. The nucleic acid may be isolated from a dicotyledonous species, preferably from the family *Brassicaceae*, further preferably from *Arabidopsis thaliana*. More preferably, the CAK isolated from *Arabidopsis thaliana* is a D-type CDK, such as a CDKD;1, CDKD;2 or a CDKD;3. The CAK isolated from *Arabidopsis thaliana* may also be a CDKF;1 from *Arabidopsis thaliana*, particularly the nucleic acid sequence as represented by SEQ ID NO: 3 and the amino acid sequence as represented by SEQ ID NO: 4. Most preferably, the CAK is CDKD;1 from *Arabidopsis thaliana*, particularly the nucleic acid sequence as represented by SEQ ID NO: 1 and the amino acid sequence as represented by SEQ ID NO: 2.

The sequence represented by SEQ ID NO: 1 depicts a CDKD;1 (a CAK) from *Arabidopsis thaliana*, with SEQ ID NO: 2 being the corresponding amino acid sequence. The sequence represented by SEQ ID NO: 3 depicts a CDKF;1 (a CAK) from *Arabidopsis thaliana*, with SEQ ID NO: 4 being the corresponding amino acid sequence. Advantageously, the applicability of the present invention is not restricted to the use of a CDKD;1 from *Arabidopsis* as represented by SEQ ID NO: 1 nor is the applicability of the present invention restricted to the use of a CDKF;1 from *Arabidopsis* as represented by SEQ ID NO: 3. The methods according to the present invention may also be practised using functional variants of the nucleic acid sequence represented by SEQ ID NO: 1 or SEQ ID NO: 3 or functional variants of the amino acid

sequence represented by SEQ ID NO: 2 or SEQ ID NO: 4. The functional variants are those which retain the ability to phosphorylate and activate CDKs and/or which are capable of modifying plant growth characteristics upon introduction in a plant. A person skilled in the art may readily determine whether or not a particular variant is functional by assaying for kinase activity on, for example, purified substrates such as human CDK2 or on the *Arabidopsis thaliana* RNA polymerase II carboxy-terminus. The ability of a CDKD functional variant to bind to cyclin H may readily be determined by co-precipitation of CAK-cyclin H complexes from purified CAK and cyclin H, or by using a two hybrid assay. A person skilled in the art may also readily determine whether a particular variant is functional (in the sense of whether it is able to modify plant growth characteristics) by simply substituting the sequence described in the Examples section below with the variant to be tested for function.

Suitable variant nucleic acid and amino acid sequences useful in practising the method according to the invention, include:

(i) Functional portions of a nucleic acid represented by the sequence of SEQ ID NO: 1 or SEQ ID NO: 3;

(ii) Sequences capable of hybridising to a nucleic acid represented by the sequence of SEQ ID NO: 1 or SEQ ID NO: 3;

(iii) Alternative splice variants of a nucleic acid represented by the sequence of SEQ ID NO: 1 or SEQ ID NO: 3;

(iv) Allelic variants of a nucleic acid represented by the sequence of SEQ ID NO: 1 or SEQ ID NO: 3; and

(v) Homologues, derivatives and active fragments of an amino acid represented by the sequence of SEQ ID NO: 2 or SEQ ID NO: 4.

Each of the aforementioned variants is a functional variant in the sense that the variant either encodes a CAK which retains the ability to phosphorylate and activate CDKs or is a CAK which retains the ability to phosphorylate and activate CDKs.

It will be apparent to a person skilled in the art that the use of the full length CAK DNA sequence would not be a prerequisite to carrying out the methods according to the invention. The methods according to the invention may advantageously be practised using functional portions of the CAK-encoding DNA/nucleic acid represented by SEQ ID NO: 1 or SEQ ID NO: 3. A functional portion refers to a piece of DNA derived or prepared from an original (larger) DNA molecule, which portion encodes a protein which is capable of phosphorylating and activating CDKs. A portion may be prepared, for example, by making one or more deletions to the nucleic acid sequence of SEQ ID NO: 1 or SEQ ID NO: 3 using techniques well known in

the art. Portions suitable for use in the methods according to the invention may readily be determined as described hereinbefore. Portions of SEQ ID NO: 1 particularly suitable in the methods of the invention include those retaining at least the motif NXTALRE, wherein X is any amino acid.

Therefore according to the invention, there is provided, a method for modifying the growth characteristics of plants, comprising introducing into a plant a portion of a nucleic acid as represented by SEQ ID NO: 1 or SEQ ID NO: 3.

Another variant sequence of SEQ ID NO: 1 or SEQ ID NO: 3 is nucleic acids capable of hybridising with the sequence represented by SEQ ID NO: 1 or SEQ ID NO: 3. Advantageously, the methods according to the present invention may also be practised using sequences that hybridise to SEQ ID NO: 1 or SEQ ID NO: 3. Hybridising sequences suitable for use in the methods according to the invention may readily be determined as described hereinbefore.

The term "hybridisation" as defined herein is a process wherein substantially homologous complementary nucleotide sequences anneal to each other. The hybridisation process can occur entirely in solution, i.e. both complementary nucleic acids are in solution. Tools in molecular biology relying on such a process include the polymerase chain reaction (PCR; and all methods based thereon), subtractive hybridisation, random primer extension, nuclease S1 mapping, primer extension, reverse transcription, cDNA synthesis, differential display of RNAs, and DNA sequence determination. The hybridisation process can also occur with one of the complementary nucleic acids immobilised to a matrix such as magnetic beads, Sepharose beads or any other resin. Tools in molecular biology relying on such a process include the isolation of poly (A^+) mRNA. The hybridisation process can furthermore occur with one of the complementary nucleic acids immobilised to a solid support such as a nitro-cellulose or nylon membrane or immobilised by e.g. photolithography to, for example, a siliceous glass support (the latter known as nucleic acid arrays or microarrays or as nucleic acid chips). Tools in molecular biology relying on such a process include RNA and DNA gel blot analysis, colony hybridisation, plaque hybridisation, *in situ* hybridisation and microarray hybridisation. In order to allow hybridisation to occur, the nucleic acid molecules are generally thermally or chemically denatured to melt a double strand into two single strands and/or to remove hairpins or other secondary structures from single stranded nucleic acids. The stringency of hybridisation is influenced by conditions such as temperature, salt concentration and hybridisation buffer composition. Hybridisation preferably occurs under stringent conditions. Stringent conditions are those that (1) employ low ionic strength and high temperature for washing, for example,

0.5M sodium phosphate buffer pH 7.2, 1mM EDTA pH 8.0 in 7% SDS at either 65°C or 55°C, or (2) employ during hybridization a denaturing agent such as formamide, for example, 50% (vol/vol) formamide with 0.1% bovine serum albumin, 0.1% Ficoll, 0.1% polyvinylpolypyrrolidone, 0.05 M sodium phosphate buffer at pH 6.5 with 0.75 M NaCl, 0.075 M sodium citrate at 42°C. A specific example includes the use of 50% formamide, 5XSSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5X Denhard's solution, sonicated salmon sperm DNA (50nm/ml), 0.1% SDS and 10% dextran sulfate at 55°C, with washes at 55°C in 0.2XSSC and 0.1% SDS. A skilled person can readily determine and vary the stringency conditions appropriately to obtain a clear and detectable hybridization signal.

Therefore according to the invention, there is provided, a method for modifying the growth characteristics of plants, comprising introducing into a plant a sequence capable of hybridising under stringent conditions to a nucleic acid sequence as represented by SEQ ID NO: 1 or SEQ ID NO: 3.

Another variant useful in the methods of the invention is an alternative splice variant of a nucleic acid as represented by the sequence of SEQ ID NO: 1 or SEQ ID NO: 3. The term "alternative splice variant" as used herein encompasses variants of a nucleic acid in which selected introns and/or exons have been excised, replaced or added. Such variants will be ones in which the biological activity of the protein remains unaffected, which can be achieved by selectively retaining functional segments of the protein. Such splice variants may be found in nature or may be manmade. Methods for making such splice variants are well known in the art. Splice variants of SEQ ID NO: 1 or SEQ ID NO: 3 suitable for use in the methods according to the invention may readily be determined as described hereinbefore.

Therefore, the invention also provides a method for modifying the growth characteristics of plants, comprising introducing into a plant an alternative splice variant of a nucleic acid as represented by SEQ ID NO: 1 or SEQ ID NO: 3.

Another variant useful in the methods of the invention is an allelic variant of a nucleic acid as represented by the sequence of SEQ ID NO: 1 or SEQ ID NO: 3. Allelic variants exist in nature and encompassed within the methods of the present invention is the use of these natural alleles. Allelic variants encompass Single Nucleotide Polymorphisms (SNPs), as well as Small Insertion/Deletion Polymorphisms (INDELs). The size of INDELs is usually less than 100 bp. SNPs and INDELs form the largest set of sequence variants in naturally occurring polymorphic strains of most organisms. Allelic variants of SEQ ID NO: 1 or SEQ ID NO: 3

suitable for use in the methods according to the invention may readily be determined as described hereinbefore.

Therefore, the invention also provides a method for modifying the growth characteristics of plants, comprising introducing into a plant an allelic variant of a nucleic acid as represented by SEQ ID NO: 1 or SEQ ID NO: 3.

Further advantageously, the methods according to the present invention may also be practised using homologues, derivatives or active fragments of a CAK as represented by SEQ ID NO: 2 or SEQ ID NO: 4. Nucleic acids encoding homologues, derivatives or active fragments of an amino acid as represented by SEQ ID NO: 2 or SEQ ID NO: 4 may readily be determined using routine techniques well known to persons skilled in the art. Such nucleic acids suitable for use in the methods of the invention may readily be determined as described hereinbefore.

"Homologues" of a protein encompass peptides, oligopeptides, polypeptides, proteins and enzymes having amino acid substitutions, deletions and/or insertions relative to the unmodified protein in question and having similar biological and functional activity as the unmodified protein from which they are derived. To produce such homologues, amino acids of the protein may be replaced by other amino acids having similar properties (such as similar hydrophobicity, hydrophilicity, antigenicity, propensity to form or break α-helical structures or β-sheet structures). Conservative substitution tables are well known in the art (see for example Creighton (1984) Proteins. W.H. Freeman and Company).

The homologues useful in the method according to the invention have in increasing order of preference at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% sequence identity to the amino acid sequence as represented by SEQ ID NO: 2. CDKDs show about 65% identity to each other and show less than 40% identity to other CDKs. Therefore a homologue having at least 50% identity to the CDK as represented by SEQ ID NO: 2 will not encompass any other CDK other than a D-type CDK.

Also encompassed by the term "homologues" are two special forms of homology, which include orthologous sequences and paralogous sequences, which encompass evolutionary concepts used to describe ancestral relationships of genes. The term "paralogous" relates to gene-duplications within the genome of a species leading to paralogous genes. The term "orthologous" relates to homologous genes in different organisms due to ancestral relationship.

Othologues in, for example, monocot plant species may easily be found by performing a so-called reciprocal blast search. This may be done by a first blast involving blasting the sequence in question (for example, SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3 or SEQ ID NO: 4) against any sequence database, such as the publicly available NCBI database which may be found at: http://www.ncbi.nlm.nih.gov. If orthologues in rice were sought, the sequence in question would be blasted against, for example, the 28,469 full-length cDNA clones from *Oryza sativa* Nipponbare available at NCBI. BLASTn may be used when starting from nucleotides or TBLASTX when starting from the protein, with standard default values (expectation 10, alignment 50). The blast results may be filtered. The full-length sequences of either the filtered results or the non-filtered results are then blasted back (second blast) against the sequence in question (SEQ ID NO: 1, 2, 3 or 4). The results of the first and second blasts are then compared. In the case of large families, ClustalW is used followed by a neighbour joining tree to help visualize the clustering.

A homologue may be in the form of a "substitutional variant" of a protein, i.e. where at least one residue in an amino acid sequence has been removed and a different residue inserted in its place. Amino acid substitutions are typically of single residues, but may be clustered depending upon functional constraints placed upon the polypeptide; insertions will usually be of the order of about 1 to 10 amino acid residues, and deletions will range from about 1 to 20 residues. Preferably, amino acid substitutions comprise conservative amino acid substitutions.

A homologue may also be in the form of an "insertional variant" of a protein, i.e. where one or more amino acid residues are introduced into a predetermined site in a protein. Insertions may comprise amino-terminal and/or carboxy-terminal fusions as well as intra-sequence insertions of single or multiple amino acids. Generally, insertions within the amino acid sequence will be smaller than amino- or carboxy-terminal fusions, of the order of about 1 to 10 residues. Examples of amino- or carboxy-terminal fusion proteins or peptides include the binding domain or activation domain of a transcriptional activator as used in the yeast two-hybrid system, phage coat proteins, (histidine)6-tag, glutathione S-transferase-tag, protein A, maltose-binding protein, dihydrofolate reductase, Tag·100 epitope, c-myc epitope, FLAG®-epitope, lacZ, CMP (calmodulin-binding peptide), HA epitope, protein C epitope and VSV epitope.

Homologues in the form of "deletion variants" of a protein are characterised by the removal of one or more amino acids from a protein.

Amino acid variants of a protein may readily be made using peptide synthetic techniques well known in the art, such as solid phase peptide synthesis and the like, or by recombinant DNA

manipulations. Methods for the manipulation of DNA sequences to produce substitution, insertion or deletion variants of a protein are well known in the art. For example, techniques for making substitution mutations at predetermined sites in DNA are well known to those skilled in the art and include M13 mutagenesis, T7-Gen *in vitro* mutagenesis (USB, Cleveland, OH), QuickChange Site Directed mutagenesis (Stratagene, San Diego, CA), PCR-mediated site-directed mutagenesis or other site-directed mutagenesis protocols.

"Derivatives" include peptides, oligopeptides, polypeptides, proteins and enzymes which may comprise substitutions, deletions or additions of naturally and non-naturally occurring amino acid residues compared to the amino acid sequence of a naturally-occurring form of the protein, for example, as presented in SEQ ID NO: 2 or SEQ ID NO: 4. "Derivatives" of a protein encompass peptides, oligopeptides, polypeptides, proteins and enzymes which may comprise naturally occurring altered, glycosylated, acylated or non-naturally occurring amino acid residues compared to the amino acid sequence of a naturally-occurring form of the polypeptide. A derivative may also comprise one or more non-amino acid substituents compared to the amino acid sequence from which it is derived, for example a reporter molecule or other ligand, covalently or non-covalently bound to the amino acid sequence, such as a reporter molecule which is bound to facilitate its detection, and non-naturally occurring amino acid residues relative to the amino acid sequence of a naturally-occurring protein.

"Active fragments" of a CAK protein encompasses at least five contiguous amino acid residues of a protein, which residues retain similar biological and/or functional activity to the naturally occurring protein, i.e. the ability to phosphorylate and activate CDKs (and RNA polymerase II).

Methods for the search and identification of CAK homologues would be well within the realm of a person skilled in the art. Methods for the alignment of sequences for comparison are well known in the art, such methods include GAP, BESTFIT, BLAST, FASTA and TFASTA. GAP uses the algorithm of Needleman and Wunsch (J. Mol. Biol. 48: 443-453, 1970) to find the alignment of two complete sequences that maximises the number of matches and minimises the number of gaps. The BLAST algorithm calculates percent sequence identity and performs a statistical analysis of the similarity between the two sequences. The software for performing BLAST analysis is publicly available through the National Centre for Biotechnology Information. Homologues suitable for use in the methods of the invention, i.e. those having at least 50% sequence identity to the amino acid sequence represented by SEQ ID NO: 2, may be identified by taking full length CDK protein sequences and aligning them using the ClustalX1.81 software using default parameters. A distance matrix may then be calculated

from this alignment using BOXSHADE software, again using default parameters. Both software programs are publicly available.

Therefore, the invention also provides a method for modifying the growth characteristics of plants, comprising modulating expression in a plant of a nucleic acid encoding a homologue, derivative or active fragment of a CAK as represented by SEQ ID NO: 2, which homologue, derivative or active fragment has in increasing order of preference at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% sequence identity to an amino acid sequence as represented by SEQ ID NO: 2.

The invention also provides genetic constructs and vectors to facilitate introduction and/or expression of the nucleotide sequences useful in the methods according to the invention.

Therefore, there is provided a gene construct comprising:

(i) a nucleic acid as represented by SEQ ID NO: 1 or SEQ ID NO: 3 or a variant of either (as defined hereinabove);

(ii) one or more control sequences capable of driving expression of the nucleic acid sequence of (i); and optionally

(iii) a transcription termination sequence.

Constructs useful in the methods according to the present invention may be constructed using recombinant DNA technology well known to persons skilled in the art. The gene constructs may be inserted into vectors, which may be commercially available, suitable for transforming into plants and suitable for expression of the gene of interest in the transformed cells.

Plants are transformed with a vector comprising the sequence of interest (i.e., a nucleic acid as represented by SEQ ID NO: 1 or SEQ ID NO: 3 or a variant of either (as defined hereinabove)). The sequence of interest is operably linked to one or more control sequences (at least to a promoter). The terms "regulatory element", "control sequence" and "promoter" are all used interchangeably herein and are to be taken in a broad context to refer to regulatory nucleic acid sequences capable of effecting expression of the sequences to which they are ligated. Encompassed by the aforementioned terms are transcriptional regulatory sequences derived from a classical eukaryotic genomic gene (including the TATA box which is required for accurate transcription initiation, with or without a CCAAT box sequence) and additional regulatory elements (i.e. upstream activating sequences, enhancers and silencers) which alter gene expression in response to developmental and/or external stimuli, or in a tissue-specific manner. Also included within the term is a transcriptional regulatory sequence of a classical

prokaryotic gene, in which case it may include a –35 box sequence and/or –10 box transcriptional regulatory sequences. The term "regulatory element" also encompasses a synthetic fusion molecule or derivative which confers, activates or enhances expression of a nucleic acid molecule in a cell, tissue or organ. The term "operably linked" as used herein refers to a functional linkage between the promoter sequence and the gene of interest, such that the promoter sequence is able to initiate transcription of the gene of interest.

Advantageously, any type of promoter may be used to drive expression of the nucleic acid sequence depending on the desired outcome. For example, a meristem-specific promoter, such as the rnr (ribonucleotide reductase), cdc2a promoter and the cyc07 promoter, may be used to effect expression in all growing parts of the plant, thereby increasing cell proliferation, which in turn would increase yield or biomass. If the desired outcome would be to influence seed characteristics, such as the storage capacity, seed size, seed number, biomass etc., then a seed-specific promoter, such as p2S2, pPROLAMIN, pOLEOSIN may be selected. An aleurone-specific promoter may be selected in order to increase growth at the moment of germination, thereby increasing the transport of sugars to the embryo. An inflorescence-specific promoter, such as pLEAFY, may be utilised if the desired outcome would be to modify the number of flower organs. To produce male-sterile plants one may use an anther specific promoter. To influence flower architecture, for example petal size, one may use a petal-specific promoter. If the desired outcome would be to modify growth and/or developmental characteristics in particular organs, then the choice of the promoter would depend on the organ to be modified. For example, use of a root-specific promoter may lead to increased growth and/or increased biomass or yield of the root and/or phenotypic alteration of the root. This may be particularly important where it is the root itself that is the desired end product; such crops include sugar beet, turnip, carrot, and potato. A fruit-specific promoter may be used to modify, for example, the strength of the outer skin of the fruit or to increase the size of the fruit. A green tissue-specific promoter may be used to increase leaf size. A cell wall-specific promoter may be used to increase the rigidity of the cell wall, thereby increasing pathogen resistance. An anther-specific promoter may be used to produce male-sterile plants. A vascular-specific promoter may be used to increase transport from leaves to seeds. A nodule-specific promoter may be used to increase the nitrogen fixing capabilities of a plant, thereby increasing nutrient levels in a plant. A stress-inducible promoter may also be used to drive expression of a nucleic acid to increase membrane integrity during conditions of stress. A stress inducible promoter such as the water stress induced promoter WSI18, the drought stress induced Trg-31 promoter, the ABA related promoter rab21 or any other promoter which is induced under a particular stress condition, such as temperature stress (cold, freezing,

heat), osmotic stress, drought stress, oxidative stress or biotic stress may be used to drive expression of a CAK gene.

Preferably, the nucleic acid encoding a CAK as represented by SEQ ID NO: 1 or SEQ ID NO: 3 or a functional variant of either is operably linked to a constitutive promoter. The term "constitutive" as defined herein refers to a promoter that is expressed predominantly in at least one tissue or organ and predominantly at any stage in the life cycle of a plant. Preferably, the constitutive promoter is expressed predominantly throughout the plant. Preferably, the constitutive promoter is the GOS2 promoter from rice.

Examples of other constitutive promoters suitable for use in the methods of the invention are listed in Table A below.

Table A: Examples of constitutive promoters for use in performance of the invention

GENE SOURCE	EXPRESSION PATTERN	REFERENCE
Actin	constitutive	McElroy *et al,* Plant Cell, 2: 163-171, 1990
CAMV 35S	constitutive	Odell *et al,* Nature, 313: 810-812, 1985
CaMV 19S	constitutive	Nilsson *et al., Physiol. Plant. 100*:456-462, 1997
GOS2	constitutive	de Pater *et al,* Plant J Nov;2(6):837-44, 1992
ubiquitin	constitutive	Christensen *et al,* Plant Mol. Biol. 18: 675-689, 1992
rice cyclophilin	constitutive	Buchholz *et al,* Plant Mol Biol. 25(5): 837-43, 1994
maize H3 histone	constitutive	Lepetit *et al,* Mol. Gen. Genet. 231:276-285, 1992
actin 2	constitutive	An *et al,* Plant J. 10(1); 107-121, 1996

Optionally, one or more terminator sequences may also be used in the construct introduced into a plant. The term "terminator" encompasses a control sequence which is a DNA sequence at the end of a transcriptional unit which signals 3' processing and polyadenylation of a primary transcript and termination of transcription. Additional regulatory elements may include transcriptional as well as translational enhancers. Those skilled in the art will be aware of terminator and enhancer sequences which may be suitable for use in performing the

invention. Such sequences would be known or may readily be obtained by a person skilled in the art.

The genetic constructs of the invention may further include an origin of replication sequence which is required for maintenance and/or replication in a specific cell type. One example is when a genetic construct is required to be maintained in a bacterial cell as an episomal genetic element (e.g. plasmid or cosmid molecule). Preferred origins of replication include, but are not limited to, the f1-ori and colE1.

The genetic construct may optionally comprise a selectable marker gene. As used herein, the term "selectable marker gene" includes any gene which confers a phenotype on a cell in which it is expressed to facilitate the identification and/or selection of cells which are transfected or transformed with a nucleic acid construct of the invention. Suitable markers may be selected from markers that confer antibiotic or herbicide resistance. Cells containing the recombinant DNA will thus be able to survive in the presence of antibiotic or herbicide concentrations that kill untransformed cells. Examples of selectable marker genes include the bar gene which provides resistance to the herbicide Basta; the npt gene which confers resistance to the antibiotic kanamycin; the hpt gene which confers hygromycin resistance. Visual markers, such as the Green Fluorescent Protein (GFP, Haseloff et al., 1997), β-glucuronidase (GUS) or luciferase may also be used as selectable markers. Further examples of suitable selectable marker genes include the ampicillin resistance (Ampr), tetracycline resistance gene (Tcr), bacterial kanamycin resistance gene (Kanr), phosphinothricin resistance gene, neomycin phosphotransferase gene (nptII), hygromycin resistance gene, gene, and the chloramphenicol acetyltransferase (CAT) gene, amongst others.

The present invention also encompasses plants obtainable by the methods according to the present invention. The present invention therefore provides plants obtainable by the method according to the present invention, which plants have modified growth characteristics and which plants have altered CAK protein activity and/or levels and/or altered expression of a nucleic acid encoding a CAK protein.

The invention also provides a method for the production of transgenic plants having modified growth characteristics, comprising introduction and expression in a plant of a nucleic acid as represented by SEQ ID NO: 1 or SEQ ID NO: 3 or a functional variant of either (as defined hereinabove).

More specifically, the present invention provides a method for the production of transgenic plants having modified growth characteristics, which method comprises:

(i) introducing into a plant or plant cell a nucleic acid as represented by SEQ ID NO: 1 or SEQ ID NO: 3 or a variant of either (as defined hereinabove;

(ii) cultivating the plant cell under conditions promoting regeneration and mature plant growth.

The nucleic acid may be introduced directly into a plant cell or into the plant itself (including introduction into a tissue, organ or any other part of a plant). According to a preferred feature of the present invention, the nucleic acid is preferably introduced into a plant by transformation.

The term "transformation" as referred to herein encompasses the transfer of an exogenous polynucleotide into a host cell, irrespective of the method used for transfer. Plant tissue capable of subsequent clonal propagation, whether by organogenesis or embryogenesis, may be transformed with a genetic construct of the present invention and a whole plant regenerated therefrom. The particular tissue chosen will vary depending on the clonal propagation systems available for, and best suited to, the particular species being transformed. Exemplary tissue targets include leaf disks, pollen, embryos, cotyledons, hypocotyls, megagametophytes, callus tissue, existing meristematic tissue (e.g., apical meristem, axillary buds, and root meristems), and induced meristem tissue (e.g., cotyledon meristem and hypocotyl meristem). The polynucleotide may be transiently or stably introduced into a host cell and may be maintained non-integrated, for example, as a plasmid. Alternatively, it may be integrated into the host genome. The resulting transformed plant cell may then be used to regenerate a transformed plant in a manner known to persons skilled in the art.

Transformation of plant species is now a fairly routine technique. Advantageously, any of several transformation methods may be used to introduce the gene of interest into a suitable ancestor cell. Transformation methods include the use of liposomes, electroporation, chemicals that increase free DNA uptake, injection of the DNA directly into the plant, particle gun bombardment, transformation using viruses or pollen and microprojection. Methods may be selected from the calcium/polyethylene glycol method for protoplasts (Krens, F.A. et al., 1882, Nature 296, 72-74; Negrutiu I. et al., June 1987, Plant Mol. Biol. 8, 363-373); electroporation of protoplasts (Shillito R.D. et al., 1985 Bio/Technol 3, 1099-1102); microinjection into plant material (Crossway A. et al., 1986, Mol. Gen Genet 202, 179-185); DNA or RNA-coated particle bombardment (Klein T.M. et al., 1987, Nature 327, 70) infection with (non-integrative) viruses and the like. Transgenic rice plants expressing a CAK are preferably produced via *Agrobacterium*-mediated transformation using any of the well known

methods for rice transformation, such as described in any of the following: published European patent application EP 1198985 A1, Aldemita and Hodges (Planta, 199, 612-617, 1996); Chan *et al.* (Plant Mol. Biol. 22 (3) 491-506, 1993), Hiei *et al.* (Plant J. 6 (2) 271-282, 1994), which disclosures are incorporated by reference herein as if fully set forth. In the case of corn transformation, the preferred method is as described in either Ishida *et al.* (Nat. Biotechnol. 1996 Jun; 14(6): 745-50) or Frame *et al.* (Plant Physiol. 2002 May; 129(1): 13-22), which disclosures are incorporated by reference herein as if fully set forth.

Generally after transformation, plant cells or cell groupings are selected for the presence of one or more markers which are encoded by plant-expressible genes co-transferred with the gene of interest, following which the transformed material is regenerated into a whole plant.

Following DNA transfer and regeneration, putatively transformed plants may be evaluated, for instance using Southern analysis, for the presence of the gene of interest, copy number and/or genomic organisation. Alternatively or additionally, expression levels of the newly introduced DNA may be monitored using Northern and/or Western analysis, both techniques being well known to persons having ordinary skill in the art.

The generated transformed plants may be propagated by a variety of means, such as by clonal propagation or classical breeding techniques. For example, a first generation (or T1) transformed plant may be selfed to give homozygous second generation (or T2) transformants, and the T2 plants further propagated through classical breeding techniques.

The generated transformed organisms may take a variety of forms. For example, they may be chimeras of transformed cells and non-transformed cells; clonal transformants (e.g., all cells transformed to contain the expression cassette); grafts of transformed and untransformed tissues (e.g., in plants, a transformed rootstock grafted to an untransformed scion).

The present invention clearly extends to any plant cell or plant produced by any of the methods described herein, and to all plant parts and propagules thereof. The present invention extends further to encompass the progeny of a primary transformed or transfected cell, tissue, organ or whole plant that has been produced by any of the aforementioned methods, the only requirement being that progeny exhibit the same genotypic and/or phenotypic characteristic(s) as those produced in the parent by the methods according to the invention. The invention also includes host cells containing an isolated nucleic acid molecule encoding a protein capable of modulating a CAK protein, preferably wherein the protein is a CAK protein. Preferred host

cells according to the invention are plant cells. The invention also extends to harvestable parts of a plant such as but not limited to seeds, leaves, fruits, flowers, rhizomes, tubers and bulbs.

The present invention also encompasses the use of nucleic acids encoding CAKs and the use of CAK polypeptides.

One such use of course relates to the use of a CAK in modifying the growth characteristics of plants, in particular in improving yield, especially seed yield. The seed yield may include one or more of the following: increased number of filled seeds, increased seed weight, increased harvest index and increased TKW, among others. The CAK may be a nucleic acid as represented by SEQ ID NO: 1 or SEQ ID NO: 3, or a variant of either as hereinbefore defined; or the CAK may be an amino acid as represented by SEQ ID NO: 2 or SEQ ID NO: 4 or a variant of either as hereinbefore defined.

Nucleic acids encoding CAKs and CAK polypeptides may also find use in breeding programmes. The CAK may be a nucleic acid as represented by SEQ ID NO: 1 or SEQ ID NO: 3, or a variant of either as hereinbefore defined; or the CAK may be an amino acid as represented by SEQ ID NO: 2 or SEQ ID NO: 4 or a variant of either as hereinbefore defined. For example, the CAK-encoding nucleic acid or a part thereof may be on a chromosome (or a part thereof), preferably together with one or more related family members. In an example of such a breeding programme, a DNA marker is identified which may be genetically linked to a gene capable of modulating expression of a nucleic acid encoding a CAK protein in a plant, which gene may be a gene encoding the CAK protein itself or any other gene which may directly or indirectly influence expression of a gene encoding a CAK protein and/or activity of the CAK protein itself. This DNA marker may then used in breeding programs to select plants having altered growth characteristics.

Allelic variants of a CAK may also be used in conventional breeding programmes, such as in marker-assisted breeding. Such breeding programmes sometimes require the introduction of allelic variations in the plants by mutagenic treatment of a plant. One suitable mutagenic method is EMS mutagenesis. Identification of allelic variants then takes place by, for example, PCR. This is followed by a selection step for selection of superior allelic variants of the sequence in question and which give rise to altered growth characteristics in a plant. Selection is typically carried out by monitoring growth performance of plants containing different allelic variants of the sequence in question, for example, different allelic variants of SEQ ID NO: 1 or SEQ ID NO: 3. Monitoring growth performance can be done in a greenhouse or in the field. Further optional steps include crossing plants, in which the superior allelic variant was

identified, with another plant. This could be used, for example, to make a combination of interesting phenotypic features.

Nucleic acids encoding CAKs and CAK polypeptides may also find use as growth regulators. The CAK may be a nucleic acid as represented by SEQ ID NO: 1 or SEQ ID NO: 3, or a variant of either as hereinbefore defined; or the CAK may be an amino acid as represented by SEQ ID NO: 2 or SEQ ID NO: 4 or a variant of either as hereinbefore defined. Since these CAKs are useful in modifying the growth characteristics of plants, the CAKs would also be useful growth regulators, such as herbicides or growth stimulators. The present invention therefore provides a composition comprising a CAK, together with a suitable carrier, diluent or excipient, for use as a growth regulator.

The methods according to the present invention result in plants having modified growth characteristics, as described hereinbefore. These advantageous growth characteristics may also be combined with other economically advantageous traits, such as further yield-enhancing traits, tolerance to various stresses, traits modifying various architectural features and/or biochemical and/or physiological features.

Description of figures

The present invention will now be described with reference to the following figures in which:

Fig. 1 is a tree showing various plant CDKs. Full-length CDK protein sequences were aligned using the "ClustalX1.81" software with its default parameters. A neighbour-joining tree was calculated from this alignment using "ClustalX1.81" with its default parameters. The tree was drawn using the "drawgram" program of the "Phylip3.5" package with its default parameters.

Fig. 2 shows a binary vector for expression in *Oryza sativa* of the *Arabidopsis thaliana* CDKD;1 gene (internal reference CDS0647) under the control of the GOS2 promoter (internal reference PRO0129).

Fig. 3 details examples of sequences useful in performing the methods according to the present invention.

Examples

The present invention will now be described with reference to the following examples, which are by way of illustration alone.

DNA manipulation: unless otherwise stated, recombinant DNA techniques are performed according to standard protocols described in (Sambrook (2001) Molecular Cloning: a laboratory manual, 3rd Edition Cold Spring Harbor Laboratory Press, CSH, New York) or in Volumes 1 and 2 of Ausubel *et al.* (1994), Current Protocols in Molecular Biology, Current Protocols. Standard materials and methods for plant molecular work are described in Plant Molecular Biology Labfase (1993) by R.D.D. Croy, published by BIOS Scientific Publications Ltd (UK) and Blackwell Scientific Publications (UK).

Example 1: Gene Cloning

The *Arabidopsis* CDKD1;1 (CDS0647) was amplified by PCR using as template an *Arabidopsis thaliana* seedling cDNA library (Invitrogen, Paisley, UK). After reverse transcription of RNA extracted from seedlings, the cDNAs were cloned into pCMV Sport 6.0. Average insert size of the bank was 1.5 kb, and original number of clones was of $1.59x10^7$ cfu. Original titer was determined to be $9.6x10^5$ cfu/ml, after first amplification of $6x10^{11}$ cfu/ml. After plasmid extraction, 200 ng of template was used in a 50 µl PCR mix. Primers prm2676 (sense, start codon in bold, AttB1 site in italic: 5' *GGGGACAAGTTTGTACAAAAAAGCAGGCTTCACA* – **ATG** GAACAGCCGAAGAAAG 3') and prm3677 (reverse, complementary, stop codon in bold, AttB2 site in italic: 5' *GGGGACCACTTTGTACAAGAAAGCTGGGT* – CCTATAGGAACTCGAGA**TCA**AGTT 3'), which include the AttB sites for Gateway recombination, were used for PCR amplification. PCR was performed using Hifi Taq DNA polymerase in standard conditions. A PCR fragment of 1256 bp was amplified and purified also using standard methods. The first step of the Gateway procedure, the BP reaction, was then performed, during which the PCR fragment recombines *in vivo* with the pDONR201 plasmid to produce, according to the Gateway terminology, an "entry clone", p2777. Plasmid pDONR201 was purchased from Invitrogen, as part of the Gateway® technology.

Example 2: Vector Construction

The entry clone p2777 was subsequently used in an LR reaction with p0640, a destination vector used for *Oryza sativa* transformation. This vector contained within the T-DNA borders: a plant selectable marker; a screenable marker; and a Gateway cassette intended for LR *in vivo* recombination with the sequence of interest already cloned in the entry clone. A rice GOS2 promoter for constitutive expression (internal reference PRO0129) was located upstream of the Gateway cassette.

After the LR recombination step, the resulting expression vector (see Figure 2) was transformed into *Agrobacterium* strain LBA4404 and subsequently to *Oryza sativa* plants.

After the LR recombination step, the resulting expression vector as shown in Figure 2 (CDK D1;1::GOS2 – upregulation) was transformed into *Agrobacterium* and subsequently into *Oryza sativa* plants. Transformed rice plants were allowed to grow and were then examined for the parameters described in Example 3.

Example 3: Evaluation and Results

Approximately 15 to 20 independent T0 rice transformants were generated. The primary transformants were transferred from tissue culture chambers to a greenhouse for growing and harvest of T1 seed. 6 events, of which the T1 progeny segregated 3:1 for presence/absence of the transgene, were retained. For each of these events, approximately 10 T1 seedlings containing the transgene (hetero- and homo-zygotes), and approximately 10 T1 seedlings lacking the transgene (nullizygotes), were selected by monitoring visual marker expression.

Statistical analysis: t-test and F-test

A two factor ANOVA (analysis of variants) was used as a statistical model for the overall evaluation of plant phenotypic characteristics. An F-test was carried out on all the parameters measured of all the plants of all the events transformed with the gene of the present invention. The F-test was carried out to check for an effect of the gene over all the transformation events and to verify for an overall effect of the gene, also known as a global gene effect. The threshold for significance for a true global gene effect was set at a 5% probability level for the F-test. A significant F-test value points to a gene effect, meaning that it is not only the presence or position of the gene that is causing the differences in phenotype.

To check for an effect of the genes within an event, i.e., for a line-specific effect, a t-test was performed within each event using data sets from the transgenic plants and the corresponding null plants. "Null plants" or "Null segregants" are the plants treated in the same way as transgenic plants, but from which the transgene has segregated. Null plants may also be described as homozygous negative transformants. The threshold for significance for the t-test was set at a 10% probability level. Within one population of 5 transformation events, some events can be under or above this t-test threshold. This is based on the hypothesis that a gene might only have an effect in certain positions in the genome, and that the occurrence of this position-dependent effect is not uncommon. This kind of gene effect is also known as a line effect of the gene. The p-value was obtained by comparing the t-value to the t-distribution or alternatively, by comparing the F-value to the F-distribution. The p-value then stands for the probability that the null hypothesis (null hypothesis being "there is no effect of the transgene") is correct.

4.1 Vegetative growth measurements:

The selected T1 plants (approximately 10 with the transgene and approximately 10 without the transgene) were transferred to a greenhouse. Each plant received a unique barcode label to link unambiguously the phenotyping data to the corresponding plant. The selected T1 plants were grown on soil in 10 cm diameter pots under the following environmental settings: photoperiod= 11.5 h, daylight intensity= 30,000 lux or more, daytime temperature= 28°C or higher, night time temperature= 22°C, relative humidity= 60-70%. Transgenic plants and the corresponding nullizygotes were grown side-by-side at random positions. From the stage of sowing until the stage of maturity each plant was passed several times through a digital imaging cabinet and imaged. At each time point digital images (2048x1536 pixels, 16 million colours) were taken of each plant from at least 6 different angles. The parameters described below were derived in an automated way from all the digital images of all the plants, using image analysis software.

4.1.1 Aboveground plant area

Plant aboveground area was determined by counting the total number of pixels from aboveground plant parts discriminated from the background. This value was averaged for the pictures taken on the same time point from the different angles and was converted to a physical surface value expressed in square mm by calibration. Experiments show that the aboveground plant area measured this way correlates with the biomass of plant parts above ground. The best 3 lines of the T1 evaluation were then evaluated in the T2 round. The results of the T2 evaluation are shown in Table 1 below. As shown, one of the lines shows a statistically significant increase in aboveground area (with p-value from the t-test of 0.0107) compared to corresponding nullizygotes.

Table 1

Aboveground Area					
Line	**TR**	**null**	**dif**	**% dif**	**p-value**
0010A	32153	27611	4541	16	0.1555
0009A	38565	30317	8249	27	0.0107
0007A	53336	56624	-3288	-6	0.3027
Overall	**41351**	**38184**	**3167**	**8**	**0.0748**

Each row corresponds to one event, for which the aboveground area was determined for the transgenics (TR) and the null lines (null), expressed in units. The numeric difference between the positive plants and the negative plants is given (dif) as well as the percentage of difference between these plants (% dif). P-value stands for the probability produced by the t-test for each plant line. The last row presents the average numbers for all events. There, the p-value stands for the p-value derived from the F-test.

4.2 Seed-related parameter measurements

The mature primary panicles were harvested, bagged, barcode-labelled and then dried for three days in the oven at 37°C. The panicles were then threshed and all the seeds were collected and counted. The filled husks were separated from the empty ones using an air-blowing device. The empty husks were discarded and the remaining fraction was counted again. The filled husks were weighed on an analytical balance. This procedure resulted in the set of seed-related parameters described below.

4.2.0 Number of filled seeds

The number of filled seeds was determined by counting the number of filled husks that remained after the separation step. Again, 3 of the best plants from the T1 evaluation were taken to the T2 round. The results of the T2 evaluation are shown in Table 2 below. As shown, 2 of the lines showed a significant increase in the number of filled seeds of transgenic plants relative to the number of filled seeds of corresponding non-transgenic plants. There was also an overall gene effect as concluded by the significant p value from the F-test of 0.

Table 2

Number of Filled Seeds					
Line	**TR**	**null**	**dif**	**% dif**	**p-value**
0010A	119	82.3	36.65	45	0.0588
0009A	146.6	18.7	127.85	684	0
0007A	198.6	207.7	-9.15	-4	0.7586
Overall	**154.7**	**102.9**	**51.78**	**50**	**0**

Each row corresponds to one event, for which the number of filled seeds was determined for the transgenics (TR) and the null lines (null), expressed in units. The numeric difference between the positive plants and the negative plants is given (dif) as well as the percentage of difference between these plants (% dif). P-value stands for the probability produced by the t-test for each plant line. The last row presents the average numbers for all events. There, the p-value stands for the p-value derived from the F-test.

4.2.1 Total seed yield per plant

The total seed yield was measured by weighing all filled husks harvested from a plant. Again, 3 of the best plants from the T1 evaluation were taken to the T2 round. The results of the T2 evaluation are shown in Table 3 below. As shown, 2 of the lines showed a significant increase in seed weight for transgenic plants relative to the seed weight of corresponding non-transgenic plants. There was also an overall gene effect as concluded by the significant p value from the F-test of 0.

Table 3

Total Seed Weight					
Line	**TR**	**null**	**dif**	**% dif**	**p-value**
0010A	3.1	2.1	0.94	44	0.0745
0009A	4	0.5	3.51	702	0
0007A	5.3	5.6	-0.36	-6	0.6589
Overall	**4.1**	**2.8**	**1.35**	**49**	**0**

Each row corresponds to one event, for which the total seed weight was determined for the transgenics (TR) and the null lines (null), expressed in units. The numeric difference between the positive plants and the negative plants is given (dif) as well as the percentage of difference between these plants (% dif). P-value stands for the probability produced by the t-test for each plant line. The last row presents the average numbers for all events. There, the p-value stands for the p-value derived from the F-test.

4.2.3 Harvest index of plants

The harvest index in the present invention is defined as the ratio between the total seed yield and the above ground area (mm^2), multiplied by a factor 106. Three of the best plants from the T1 evaluation were taken to the T2 round and the results of the T2 evaluation are shown in Table 4 below. As shown, 1 line showed an increased harvest index for transgenic plants relative to the harvest index of corresponding non-transgenic plants, with a p value from the t-test of 0. An overall gene effect was also evident with a p-value from the F-test of 0.

Table 4

Harvest Index					
Line	**TR**	**null**	**dif**	**% dif**	**p-value**
0010A	95.8	86.3	9.47	11	0.3758
0009A	104.1	18.1	85.93	473	0
0007A	94.6	94.7	-0.14	-0	0.9885
Overall	**97.9**	**68.6**	**29.27**	**43**	**0**

Each row corresponds to one event, for which the harvest index was determined for the transgenics (TR) and the null lines (null), expressed in units. The numeric difference between the positive plants and the negative plants is given (dif) as well as the percentage of difference between these plants (% dif). P-value stands for the probability produced by the t-test for each plant line. The last row presents the average numbers for all events. There, the p-value stands for the p-value derived from the F-test.

4.2.4 Thousand Kernel Weight (TKW)

This parameter is extrapolated from the number of filled seeds counted, and their total weight. Three of the best plants from the T1 evaluation were taken to the T2 round and the

results of the T2 evaluation are shown in Table 5 below. As shown, one of the lines showed an increase in the TKW for transgenic plants relative to corresponding non-transgenic plants, with a p value from the t-test of 0.0455.

Table 5

TKW					
Line	**TR**	**null**	**dif**	**% dif**	**p-value**
OS0934-0010A	25.1	24.6	0.52	2	0.3453
OS0934-0009A	26.1	24.8	1.23	5	0.0455
OS0934-0007A	26.5	26.8	-0.3	-1	0.5609
Overall	**25.9**	**25.5**	**0.39**	**2**	**0.2473**

Example 4: Application of the invention in maize

The methods according to the invention may also be used to modify the growth characteristics of maize. A CAK is cloned under control of a constitutive promoter in a plant transformation vector suited for *Agrobacterium*-mediated corn transformation. Such vectors and methods for corn transformation have been described in literature (EP0604662, EP0672752, EP0971578, EP0955371, EP0558676, Ishida *et al.* 1996; Frame *et al.*, 2002).

Transgenic plants made by these methods are grown in the greenhouse for T1 seed production. Inheritability and copy number of the transgene is checked by quantitative real-time PCR and Southern blot analysis and expression levels of the transgene is determined by reverse PCR and Northern analysis. Transgenic lines with single copy insertions of the transgene and with varying levels of transgene expression are selected for T2 seed production. Progeny seeds are germinated and grown in the greenhouse in conditions adapted for maize (16:8 photoperiod, 26-28°C daytime temperature and 22-24°C nighttime temperature) as well under water-deficient, nitrogen-deficient, and excess NaCl conditions.

In the case of selfing, null segregants from the same parental line, as well as wild type plants of the same cultivar are used as controls. The progeny plants resulting from the selfing or crosses are evaluated for different biomass and growth parameters, including plant height, stalk/stem thickness, number of leaves, total above ground area, leaf greenness, time to maturity, time to silking, flowering time, ear number, ear length, row number, kernel number, kernel size, kernel oil content, grain maturity, harvest time. Lines that are most significantly improved for any of the above-mentioned parameters are selected for further field-testing and marker-assisted breeding, with the objective of transferring the field-validated transgenic traits into commercial germplasm. Methods for testing maize for growth and yield-related parameters in the field are well established in the art, as are techniques for introgressing

specific loci (such as transgene containing loci) from one germplasm into another. This also includes transferring a trait(s) of interest from a transformed inbred line to a commercial hybrid with desirable added agronomic or nutritional or medical value.

5

Claims

1. Method for modifying plant growth characteristics, comprising introducing into a plant a nucleic acid encoding a CAK.

2. Method according to claim 1, wherein said modified plant growth characteristics is increased yield relative to corresponding wild type plants.

3. Method according to claim 2, wherein said increased yield is increased seed yield.

4. Method according to claim 2 or 3, wherein said increased yield is selected from the group consisting of (i) increased biomass of one or more parts of a plant; (ii) increased seed biomass; (iii) increased number of (filled) seeds; (iv) increased seed size; (v) increased seed volume; (vi) increased harvest index; and (vii) increased thousand kernel weight (TKW).

5. Method according to any of one of claims 1 to 4, wherein said modified plant growth characteristics comprises increased growth rate.

6. Method according to claim any one of claims 1 to 5, wherein said nucleic acid encoding a CAK is obtained from a plant.

7. Method according to claim and one of claims 1 to 6, wherein said nucleic acid encoding a CAK is a D-type CDK or an F-type CDK-encoding nucleic acid.

8. Method according to any one of claims 1 to 7, wherein said nucleic acid encoding a CAK is represented by SEQ ID NO: 1 or SEQ ID NO: 3 or a functional variant of either and wherein the CAK polypeptide is represented by SEQ ID NO: 2 or SEQ ID NO: 4 or a functional variant of either, which functional variant is selected from the group consisting of:
   (i) Functional portions of a nucleic acid represented by the sequence of SEQ ID NO: 1 or SEQ ID NO: 3;
   (ii) Sequences capable of hybridising to a nucleic acid represented by the sequence of SEQ ID NO: 1 or SEQ ID NO: 3;
   (iii) Alternative splice variants of a nucleic acid represented by the sequence of SEQ ID NO: 1 or SEQ ID NO: 3;

(iv) Allelic variants of a nucleic acid represented by the sequence of SEQ ID NO: 1 or SEQ ID NO: 3; and

(v) Homologues, derivatives and active fragments of an amino acid represented by the sequence of SEQ ID NO: 2 or SEQ ID NO: 4.

9. Method according to any one of claims 1 to 8, wherein said nucleic acid sequence encoding a CAK is overexpressed in a plant.

10. Method according to any one of claims 1 to 9, wherein expression of said nucleic acid encoding a CAK is driven by a constitutive promoter.

11. Method for the production of a transgenic plant having modified growth characteristics, which method comprises:

(i) introducing into a plant or plant cell a nucleic acid as represented by SEQ ID NO: 1 or SEQ ID NO: 3 or a functional variant of either;

(ii) cultivating the plant cell under conditions promoting regeneration and mature plant growth.

12. Method according to claim 11, wherein said modified growth characteristics comprises increased seed yield.

13. Plants obtainable by a method according to any of claims 1 to 12.

14. Construct comprising:

(i) a nucleic acid as represented by SEQ ID NO: 1 or SEQ ID NO: 3 or a functional variant of either;

(ii) one or more control sequence capable of driving expression of the nucleic acid sequence of (i); and optionally

(iii) a transcription termination sequence.

15. Construct according to claim 14, wherein said control sequences comprises a constitutive promoter.

16. Plant transformed with a construct according to claim 14 or 15.

17. Transgenic plant having modified growth characteristics, characterised in that said plant comprises an isolated nucleic acid encoding a CAK.

18. Transgenic plant according to claim 13, 16 or 17, wherein said plant is a monocotyledonous plant, such as sugar cane or wherein said plant is a cereal, such as rice, maize, wheat, barley, millet, rye or oats.

19. Harvestable parts of a plant according to any one of claims 13 or 16 to 18.

20. Use of an isolated nucleic acid encoding a CAK protein in modifying the growth characteristics of plants, in particular in improving yield, especially seed yield.

21. Use according to claim 20, wherein said seed yield includes one or more of the following: increased number of filled seeds, increased seed weight, increased harvest index and increased TKW.

22. Use according to claim 20 or 22, wherein said CAK is a nucleic acid as represented by SEQ ID NO: 1 or SEQ ID NO: 3 or a functional variant of either, or wherein said CAK is an amino acid as represented by SEQ ID NO: 2 or SEQ ID NO: 4 or a functional variant of either.

Abstract

Plants having modified growth characteristics and method for making the same

The present invention concerns a method for modifying the growth characteristics of plants by introducing into a plant a nucleic acid encoding a CAK. The invention also plants produced by the methods of the invention and to constructs useful in such methods.

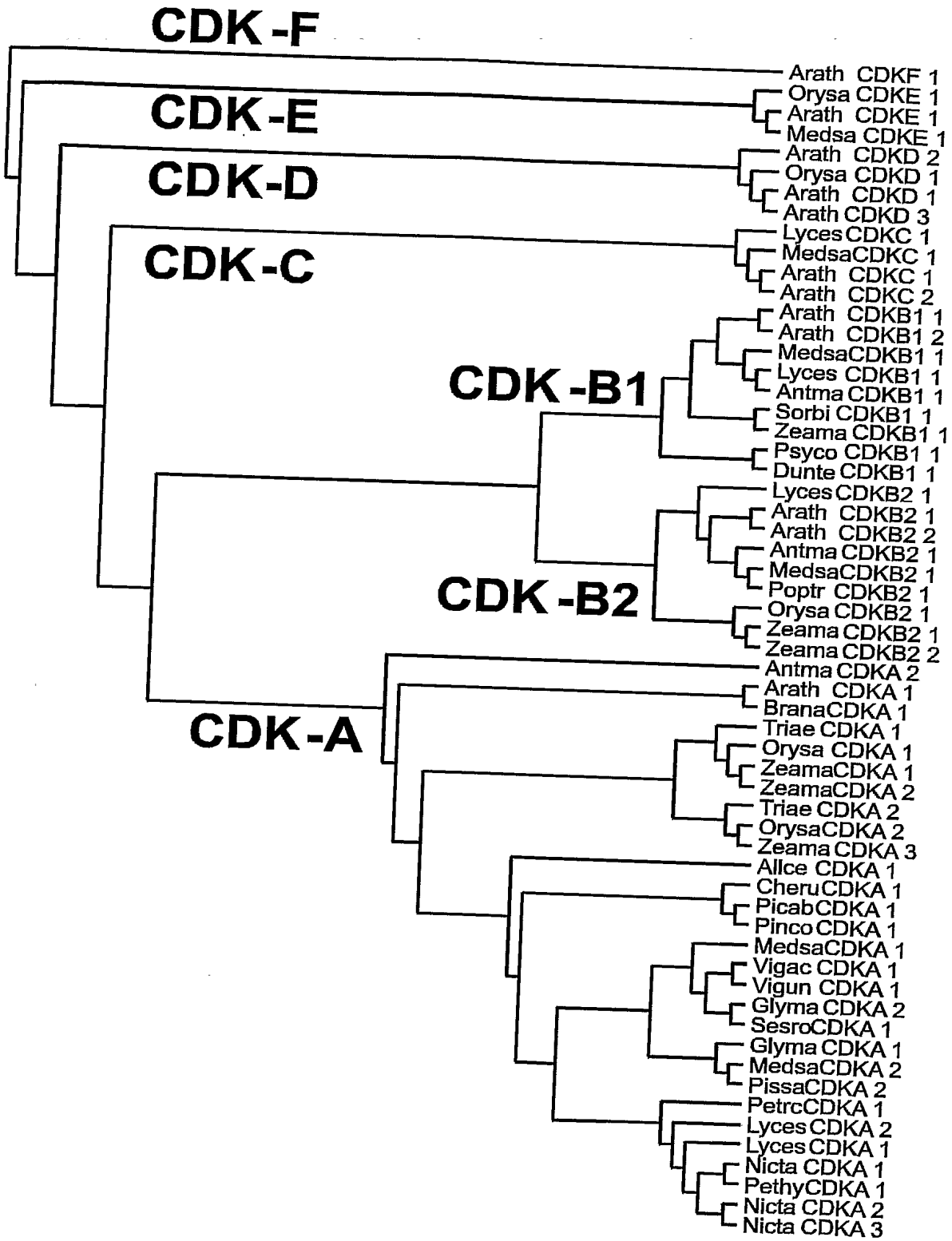
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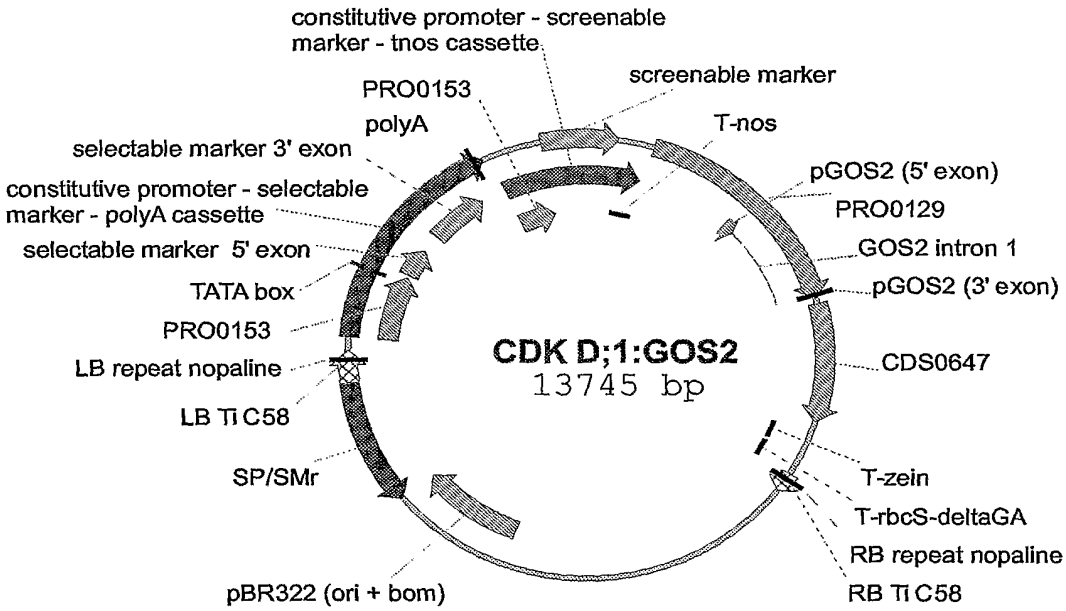
FIGURE1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PRO0129
selectable marker 5' exon
GOS2 intron 1
TATA box
pGOS2 (3' exon)
PRO0153
CDK D;1:GOS2
13745 bp
LB repeat nopaline
CDS0647
LB Ti C58
T-zein
SP/SMr
T-rbcS-deltaGA
RB repeat nopaline
pBR322 (ori + bom)
RB Ti C58

FIGURE 2

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FIGURE 3

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Seqidno 07: prm2677 reverse, complementary, stop codon in bold, AttB2 site in italic

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FIGURE 3 (continued)

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<213> Arabidopsis thaliana

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35 40 45

Glu Gly Val Asn Val Thr Ala Leu Arg Glu Ile Lys Leu Leu Lys Glu
50 55 60

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Leu Lys His Pro His Ile Ile Glu Leu Ile Asp Ala Phe Pro His Lys
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Glu Asn Leu His Ile Val Phe Glu Phe Met Glu Thr Asp Leu Glu Ala
                85                  90                  95

Val Ile Arg Asp Arg Asn Leu Tyr Leu Ser Pro Gly Asp Val Lys Ser
            100                 105                 110

Tyr Leu Gln Met Ile Leu Lys Gly Leu Glu Tyr Cys His Gly Lys Trp
        115                 120                 125

Val Leu His Arg Asp Met Lys Pro Asn Asn Leu Leu Ile Gly Pro Asn
    130                 135                 140

Gly Gln Leu Lys Leu Ala Asp Phe Gly Leu Ala Arg Ile Phe Gly Ser
145                 150                 155                 160

Pro Gly Arg Lys Phe Thr His Gln Val Phe Ala Arg Trp Tyr Arg Ala
                165                 170                 175

Pro Glu Leu Leu Phe Gly Ala Lys Gln Tyr Asp Gly Ala Val Asp Val
            180                 185                 190

Trp Ala Ala Gly Cys Ile Phe Ala Glu Leu Leu Leu Arg Arg Pro Phe
        195                 200                 205

Leu Gln Gly Asn Ser Asp Ile Asp Gln Leu Ser Lys Ile Phe Ala Ala
    210                 215                 220

Phe Gly Thr Pro Lys Ala Asp Gln Trp Pro Asp Met Ile Cys Leu Pro
225                 230                 235                 240

Asp Tyr Val Glu Tyr Gln Phe Val Pro Ala Pro Ser Leu Arg Ser Leu
                245                 250                 255

Leu Pro Thr Val Ser Glu Asp Ala Leu Asp Leu Leu Ser Lys Met Phe
            260                 265                 270

Thr Tyr Asp Pro Lys Ser Arg Ile Ser Ile Gln Gln Ala Leu Lys His
        275                 280                 285

Arg Tyr Phe Thr Ser Ala Pro Ser Pro Thr Asp Pro Leu Lys Leu Pro
    290                 295                 300

Arg Pro Val Ser Lys Gln Asp Ala Lys Ser Ser Asp Ser Lys Leu Glu
305                 310                 315                 320

Ala Ile Lys Val Leu Ser Pro Ala His Lys Phe Arg Arg Val Met Pro
                325                 330                 335

Asp Arg Gly Lys Ser Gly Asn Gly Phe Lys Asp Gln Ser Val Asp Val
            340                 345                 350

Met Arg Gln Ala Ser His Asp Gly Gln Ala Pro Met Ser Leu Asp Phe
        355                 360                 365

Thr Ile Leu Ala Glu Arg Pro Pro Asn Arg Pro Thr Ile Thr Ser Ala
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Ala Asp Val Tyr Arg Ala Arg Arg Leu Ser Asp Gly Leu Ile Val Ala
35 40 45

Leu Lys Glu Ile Phe Asp Tyr Gln Ser Ala Phe Arg Glu Ile Asp Ala
50 55 60

Leu Thr Ile Leu Asn Gly Ser Pro Asn Val Val Val Met His Glu Tyr
65 70 75 80

Phe Trp Arg Glu Glu Glu Asn Ala Val Leu Val Leu Glu Phe Leu Arg
85 90 95

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Ser Asp Leu Ala Ala Val Ile Arg Asp Gly Lys Arg Lys Lys Lys Val
            100                 105                 110

Glu Gly Gly Asp Gly Phe Ser Val Gly Glu Ile Lys Arg Trp Met Ile
        115                 120                 125

Gln Ile Leu Thr Gly Val Asp Ala Cys His Arg Asn Leu Ile Val His
    130                 135                 140

Arg Asp Leu Lys Pro Gly Asn Met Leu Ile Ser Asp Asp Gly Val Leu
145                 150                 155                 160

Lys Leu Ala Asp Phe Gly Gln Ala Arg Ile Leu Met Glu His Asp Ile
                165                 170                 175

Val Ala Ser Asp Glu Asn Gln Gln Ala Tyr Lys Leu Glu Asp Lys Asp
            180                 185                 190

Gly Glu Thr Ser Glu Pro Pro Glu Val Ile Pro Asp Tyr Glu Asn Ser
        195                 200                 205

Pro Arg Gln Gly Ser Asp Gly Gln Glu Arg Glu Ala Met Ser Lys Asp
    210                 215                 220

Glu Tyr Phe Arg Gln Val Glu Glu Leu Lys Ala Lys Gln Val Val Arg
225                 230                 235                 240

Asp Asp Thr Asp Lys Asp Ser Asn Val His Asp Gly Asp Ile Ser Cys
                245                 250                 255

Leu Ala Thr Cys Thr Val Ser Glu Met Asp Asp Asp Leu Gly Arg Asn
            260                 265                 270

Ser Phe Ser Tyr Asp Ala Asp Glu Ala Val Asp Asp Thr Gln Gly Leu
        275                 280                 285

Met Thr Ser Cys Val Gly Thr Arg Trp Phe Arg Pro Pro Glu Leu Leu
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Tyr Gly Ser Thr Met Tyr Gly Leu Glu Val Asp Leu Trp Ser Leu Gly
305                 310                 315                 320

Cys Val Phe Ala Glu Leu Leu Ser Leu Glu Pro Leu Phe Pro Gly Ile
                325                 330                 335

Ser Asp Ile Asp Gln Ile Ser Arg Val Thr Asn Val Leu Gly Asn Leu
            340                 345                 350

Asn Glu Glu Val Trp Pro Gly Cys Val Asp Leu Pro Asp Tyr Lys Ser
        355                 360                 365

Ile Ser Phe Ala Lys Val Glu Ser Pro Leu Gly Ile Glu Gly Cys Leu
    370                 375                 380

Pro Asn His Ser Gly Asp Val Ile Ser Leu Leu Lys Lys Leu Ile Cys
385                 390                 395                 400

Tyr Asp Pro Ala Ser Arg Ala Thr Thr Met Glu Met Leu Asn Asp Lys
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Tyr Leu Ser Glu Glu Pro Leu Pro Val Pro Val Ser Glu Leu Tyr Val
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Pro Pro Thr Met Ser Gly Pro Asp Glu Asp Ser Pro Arg Lys Trp Asn
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Asp Tyr Arg Glu Met Asp Ser Asp Ser Asp Phe Asp Gly Phe Gly Pro
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Met Asn Val Lys Pro Thr Ser Ser Gly Phe Thr Ile Glu Phe Pro
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<213> Artificial sequence

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